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GenCore version 5.1.6

OM protein - protein search, using sw model  
Run on: March 7, 2005, 07:04:17 ; Search time 4.6765 Seconds  
(without alignments)  
1193.323 Million cell updates/sec

Title: US-09-939-537-35  
Perfect score: 288  
Sequence: 1 PRASALPAPPTGSSALPDQTV.....VISFLGLGGLGVACVLARTR 58  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216733 residues

Total number of hits satisfying chosen parameters: 283416  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:  
5:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

**ALIGNMENTS**

Result No.	Score	Query Match	Length	DB ID	Description
1	284	98.6	240	2	T-cell surface glycoprotein CD7 precursor - human
2	80	27.8	421	2	T-cell surface glycoprotein CD7 precursor - human
3	77	26.7	375	2	T-cell surface glycoprotein CD7 precursor - human
4	76.5	26.6	710	2	T-cell surface glycoprotein CD7 precursor - human
5	75	26.0	539	2	T-cell surface glycoprotein CD7 precursor - human
6	75	26.0	891	2	T-cell surface glycoprotein CD7 precursor - human
7	74	25.7	464	2	T-cell surface glycoprotein CD7 precursor - human
8	73	25.3	215	2	T-cell surface glycoprotein CD7 precursor - human
9	73	25.3	418	2	T-cell surface glycoprotein CD7 precursor - human
10	73	25.3	482	2	T-cell surface glycoprotein CD7 precursor - human
11	73	25.3	614	2	T-cell surface glycoprotein CD7 precursor - human
12	71	24.7	262	2	T-cell surface glycoprotein CD7 precursor - human
13	70.5	24.5	559	2	T-cell surface glycoprotein CD7 precursor - human
14	70.5	24.5	660	1	T-cell surface glycoprotein CD7 precursor - human
15	69.5	24.1	1249	2	T-cell surface glycoprotein CD7 precursor - human
16	69	24.0	279	2	T-cell surface glycoprotein CD7 precursor - human
17	69	24.0	405	2	T-cell surface glycoprotein CD7 precursor - human
18	69	24.0	192	2	T-cell surface glycoprotein CD7 precursor - human
19	68.5	23.8	347	2	T-cell surface glycoprotein CD7 precursor - human
20	68.5	23.8	684	2	T-cell surface glycoprotein CD7 precursor - human
21	68.5	23.8	236	2	T-cell surface glycoprotein CD7 precursor - human
22	68	23.6	801	2	T-cell surface glycoprotein CD7 precursor - human
23	68	23.6	907	2	T-cell surface glycoprotein CD7 precursor - human
24	68	23.6	1151	2	T-cell surface glycoprotein CD7 precursor - human
25	68	23.6	173	2	T-cell surface glycoprotein CD7 precursor - human
26	67.5	23.4	2240	2	T-cell surface glycoprotein CD7 precursor - human
27	67.5	23.4	231	2	T-cell surface glycoprotein CD7 precursor - human
28	67	23.4	237	2	T-cell surface glycoprotein CD7 precursor - human
29	67	23.3	377	2	T-cell surface glycoprotein CD7 precursor - human
30					gene ox40 protein
31					myoblast determina
32					proline-rich prote
33					mucin 1 precursor,
34					rod shape-determin
35					probable dihydrodi
36					related to cytoske
37					hypothetical prote
38					peptidyl-prolyl ci
39					factor VII intron
40					hypothetical prote
41					probable PBP prote
42					arabinogalactan-pr
43					18K4.10 (imported
44					hypothetical prote
45					probable membrane

**RESULT 1**

A19016 T-cell surface glycoprotein CD7 precursor - human  
N:Alternate names: T-cell leukemia antigen  
C:Species: Homo sapiens (man)  
C:Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 09-Jul-2004  
C:Accession: A19016; S03520  
R:Schanberg, L.B.; Fleenor, D.B.; Kurtzberg, J.; Haynes, B.F.; Kaufman, R.E.  
Proc. Natl. Acad. Sci., U.S.A., 88, 635-637, 1991  
A:Title: Isolation and characterization of the genomic human CD7 gene: structural similarity  
A:Reference number: A19016; MUID:9111057; PMID:1703303  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-240 <SCH>  
A:Cross-references: UNIPROT:P09564; GB:M37271; NID:9180163; PID:AA51953.1; PID:g180164  
R:Aruffo, A.; Seed, B.  
ENBIO J., 6, 3313-3316, 1987  
A:Title: Molecular cloning of two CD7 (T-cell leukemia antigen) cDNAs by a COS cell exprt  
A:Reference number: S03520; MUID:88111517; PMID:3501369  
A:Accession: S03520  
A:Molecule type: mRNA  
A:Residues: 1-240 <ARU>  
A:Cross-references: EMBL:X06180; NID:g29819; PIDN:CAA29546.1; PID:g732757  
C:Genetics:  
A:Gene: GDB:CD7  
A:Cross-references: GDB:19770; OMIM:186820  
A:Map Position: 17q25.2-17q25.3  
A:Introns: 28/1  
C:Keywords: glycoprotein; membrane protein; surface antigen; tandem repeat  
F1-25/Domain: Signal Sequence #status Predicted <SIG>  
F1-26/240/Product: T-cell surface glycoprotein CD7 #status Predicted <MAT>  
F145-180/Region: 9-residue repeats (X-P-X-A-S-L-P)  
Query Match 98.6%; Score 284; DB 2; Length 240;  
Best Local Similarity 98.3%; Pred. No. 2; 3e-19;  
Matches 57; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

#### RESULTS

**RESULT 2**

T30709 core protein homolog 107L - *Molluscum contagiosum* virus 1  
N:Alternate names: MCL017L  
C:Species: *Molluscum contagiosum* virus 1  
C:Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004  
C:Accession: T30709  
R:Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.  
Science 273, 813-816, 1996

Query Match 27.8%; Score 80; DB 2; Length 421;  
 Best Local Similarity 54.5%; Pred. No. 2;4; Mismatches 0; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 3 ASALPAPPTGSLIDPDOTASALPDPPASALPA 35  
 Db 220 APACPADATSPACPAPATAPACPATAPACPA 252

**RESULT 3**

T08134 oleosin-like protein - rape  
 C;Species: Brassica napus (rape)  
 C;Date: 21-May-1999 #sequence\_revision 21-May-1999 #text\_change 09-Jul-2004  
 C;Accession: T08134  
 R;Hong, H.P.; Robb, J.H.; Gerster, J.L.; Rigas, S.; Datla, R.S.; Hatzopoulos, P.; Scopes  
 Plant Mol. Biol. 34, 549-555, 1997  
 A;Title: Promoter sequences from two different Brassica napus tapetal oleosin-like genes  
 A;Reference number: 216373; MUID:97369377; PMID:9225865  
 A;Accession: T08134  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: DNA  
 A;Residues: 1-305 <HON>  
 A;Cross-references: UNIPROT:P93066; EMBL:Y08986; NID:91769971; PID:9176  
 A;Experimental source: cv. Jet Neuf  
 C;Genetics:  
 C;Introns: 105/2; 184/2

Query Match 26.7%; Score 77; DB 2; Length 375;  
 Best Local Similarity 47.4%; Pred. No. 4;1; Mismatches 1; Indels 0; Gaps 0;  
 Matches 18; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

Qy 1 PRASALLAPPTGSLIDPDOTASALPDPPASALPA 38  
 Db 213 PRAPAAPAAPAAPAAPAAPAAPAPEAPA 250

**RESULT 4**

D96728 hypothetical protein F24J3.3 [imported] - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C;Accession: D96728  
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.,  
 Ansen, N.F.; Hughes, B.; Hulzar, L.  
 Nature 408, 816-820, 2000  
 C;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.,  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marzali, I.,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.; Ventner, J.C.;  
 A;Title: Sequence and analysis of chromosome 2 of the Plant Arabidopsis thaliana.  
 A;Reference number: A86141; MUID:21016719; PMID:11130712  
 A;Accession: D96728  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-710 <STO>  
 A;Cross-references: UNIPROT:Q9CAL8; GB:AE005173; NID:96175155; PIDN:AF04882.1; GSPDB:GN  
 C;Genetics:  
 C;Introns: 1-710 <STO>  
 A;Gene: F24J3.3  
 A;Map position: 1

Query Match 26.0%; Score 75; DB 2; Length 891;  
 Best Local Similarity 42.9%; Pred. No. 14; Mismatches 3; Indels 6; Gaps 1;  
 Matches 15; Conservative 3; Mismatches 11; Indels 6; Gaps 1;

Qy 7 PRAP-----PQSALIDPQTASALPPPPASALPA 35  
 Db 441 PSPVARLRDPTGARLPSIQRRLPSPPVQRLPS 475

**RESULT 5**

T28770 hypothetical protein W03D2.1 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T28770  
 R;Rohlfing, T.; Wohldmann, P.  
 Submitted to the EMBL Data Library, June 1997  
 A;Description: The sequence of C. elegans  
 A;Reference number: 220519  
 A;Accession: T28770  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: DNA  
 A;Residues: 1-559 <ROH>  
 A;Cross-references: UNIPROT:Q8MNQ9; EMBL:AF000298; PIDN:AAC48255.1; GSPDB:GN00022; CESP:Y  
 C;Genetics:  
 A;Experimental source: strain Bristol N2; clone W03D2  
 A;Map position: 40/3; 88/3; 115/3; 146/3; 173/3  
 A;Introns: 40/3; 88/3; 115/3; 146/3; 173/3  
 C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology  
 Query Match 26.0%; Score 75; DB 2; Length 539;  
 Best Local Similarity 47.1%; Pred. No. 8;7; Mismatches 2; Indels 2; Gaps 1;  
 Matches 16; Conservative 2; Mismatches 14; Indels 2; Gaps 1;

Qy 1 PRASALPAPPTGSLIDPDQTMASALPDPPASALP 34  
 Db 288 PRTGSPPPPPTGS--PPPPAGGSPPPRAGSPP 319

**RESULT 6**

G84693 probable proline-rich protein [imported] - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
 C;Accession: G84693  
 R;Lin, X.; Kaul, S.; Rounaley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Yuen, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ventner, J.,  
 M.; Koo, H.; Morffat, K.S.; Cronin, L.A.; Shen, M.; Vanken, S.E.; Umeyam, L.; Tailor, L.,  
 A;Accession: G84693  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-691 <STO>  
 A;Cross-references: UNIPROT:Q9ZWW8; GB:AE002093; NID:93980411; PIDN:AAC95214.1; GSPDB:GN  
 C;Genetics:  
 A;Gene: AT2g29210  
 A;Map position: 2

Query Match 26.0%; Score 75; DB 2; Length 891;  
 Best Local Similarity 42.9%; Pred. No. 14; Mismatches 3; Indels 6; Gaps 1;  
 Matches 15; Conservative 3; Mismatches 11; Indels 6; Gaps 1;

Qy 7 PRAP-----PQSALIDPQTASALPPPPASALPA 35  
 Db 441 PSPVARLRDPTGARLPSIQRRLPSPPVQRLPS 475

**RESULT 7**

S22697 extensin - Volvox carteri (fragment)

S22697

C;Species: *Volvox carteri*  
 C;Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 09-Jul-2004  
 C;Accession: S22657; S21005  
 R;Brtl, H.; Hallmann, A.; Wenzl, S.; Sumper, M.  
 EMBO J. 11, 205-2062, 1992  
 A;Title: A novel extensin that may organize extracellular matrix biogenesis in *Volvox carteri*  
 A;Reference number: S22697; MUID:9289669; PMID:1600938  
 A;Accession: S22697  
 A;Molecule type: mRNA  
 A;Residues: 1-464 <HAL>  
 A;Cross-references: UNIPROT:Q41645; EMBL:X65165; NID:921991; PIDN:CAA46283.1; PID:g21992  
 C;Keywords: glycoprotein

Query Match 25.7%; Score 74; DB 2; Length 464;  
 Best Local Similarity 47.1%; Pred. No. 9.4;  
 Matches 16; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
 QY 1 PRASALPAPTPGSAALPDQNTASALPDPPASALP 34  
 Db 344 PRPSPSPPPRSSPSPPPVSPPPPRASPP 377

RESULT 8

S46965 microfilarial stealth protein - nematode (*Litomosoides carinii*)  
 C;Species: *Litomosoides carinii*  
 C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
 C;Accession: S46966  
 R;Hirnmann, J.; Schnauffer, A.; Hintz, M.; Conraths, F.J.; Stirn, S.; Zahner, H.; Hobom, G.;Description: *Brugia spp.* and *Litomosoides carinii*: characterization of the shp2 gene  
 A;Reference: S46964  
 A;Accession: S46966  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-215 <HHR>  
 A;Cross-references: UNIPROT:Q25256; EMBL:235443; NID:9516387; PID:9516388  
 A;Genetics: C;Intron: 19/3

Query Match 25.3%; Score 73; DB 2; Length 492;  
 Best Local Similarity 44.4%; Pred. No. 12; Mismatches 4; Indels 2; Gaps 1;  
 Matches 16; Conservative 0; Mismatches 14; Indels 2; Gaps 1;

QY 1 PRASALP--APPGSALDPDQNTASALPDPPASALP 34  
 Db 185 PTATPATATAPPVAPPTAVPPPPALASPP 220

RESULT 9

G02953 beta-3-adrenergic receptor - rhesus macaque  
 C;Species: *Macaca mulatta* (rhesus macaque)  
 C;Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 09-Jul-2004  
 C;Accession: G02953  
 R;Low, A.L.; Walston, J.; Shuldiner, A.R.; submitted to the EMBL Data Library, July 1996  
 A;Reference number: H01989  
 A;Accession: G02953  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues 1-488 <LOW>  
 A;Cross-references: UNIPROT:Q28524; EMBL:U63592; NID:91458230; PIDN:AAB53939.1; PID:g145  
 C;Genetics: C;Intron: 402/1  
 C;Superfamily: vertebrate rhodopsin

Query Match 25.3%; Score 73; DB 2; Length 418;  
 Best Local Similarity 32.1%; Pred. No. 11; Mismatches 11; Indels 0; Gaps 0;  
 Matches 18; Conservative 11; Mismatches 27; Indels 0; Gaps 0;

QY 3 ASALPAPPTGSAALPDQNTASALPDPPASALP 38  
 Db 56 APPAPAPPAAPPPAAAPAPAPAPAPAPAPA 91

RESULT 9

G02953 beta-3-adrenergic receptor - rhesus macaque  
 C;Species: *Macaca mulatta* (rhesus macaque)  
 C;Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 09-Jul-2004  
 C;Accession: G02953  
 R;Low, A.L.; Walston, J.; Shuldiner, A.R.; submitted to the EMBL Data Library, July 1996  
 A;Reference number: H01989  
 A;Accession: G02953  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues 1-488 <LOW>  
 A;Cross-references: UNIPROT:Q91INFO; GB:ABC005172; NID:g8810458; PIDN:AAF80119.1; GSPPDB:GN01  
 C;Genetics: C;Map Position: 1

Query Match 25.3%; Score 73; DB 2; Length 614;  
 Best Local Similarity 43.4%; Pred. No. 15; Mismatches 23; Conservative 5; Indels 4; Gaps 2;  
 Matches 23; Conservative 5; Mismatches 21; Indels 4; Gaps 2;

QY 3 ASALPAPPTGSAALPDQNTASALPDPPASALP 54  
 Db 94 ASALPSAVSSSSPEPEPSIAMLNDLNRLVIAAVACLGVTISFLA--GASCVL 143

RESULT 12

T06600 acetyl-CoA carboxylase (EC 6.4.1.2), biotin carboxyl carrier chain precursor - soybean  
 N;Contains: biotin carboxyl carrier chain  
 C;Species: Glycine max (soybean)  
 C;Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004  
 C;Accession: T06600  
 R;Nielsen, N.C.; Reverdatto, S.V.; Beilinson, V.A.  
 Submitted to the EMBL Data Library, November 1995

A;Reference number: 215788  
 A;Accession: T06600  
 A;Status: translated from GB/EMBL/DDJB  
 A;Molecule type: mRNA  
 A;Residues: 1-262 <NIE>  
 A;Cross-references: UNIPROT:Q42783; EMBL:U40666; NID:9143318; PIDN:AAF67836.1; PID:9114  
 A;Experimental source: strain Resnik  
 A;Genetics:  
 A;Gene: accB-1  
 A;Genome: nuclear  
 C;Complex: acetyl-CoA carboxylase is composed of biotin carboxylase (EC 6.3.4.14), carb  
 A;Description: entire acetyl-CoA carboxylase complex catalyzes synthesis of malonyl-CoA  
 carboxylation of biotin bound to biotin-carboxyl-carrier protein with bicarbonate; carb  
 A;Pathway: fatty acid biosynthesis  
 C;Function: <BCC>  
 A;Description: biotin carboxyl carrier chain is responsible for binding of biotin  
 A;Pathway: fatty acid biosynthesis  
 C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology  
 C;Keywords: biotin metabolism; chloroplast; fatty acid biosynthesis; ligase  
 P;1/47/Domain: transit peptide (chloroplast) #status predicted <TMP>  
 P;48-262/Product: acetyl-CoA carboxylase, biotin carboxyl carrier chain #status predicted  
 Query Match 24.7%; Score 71; DB 2; Length 262;  
 Best Local Similarity 41.7%; Pred. No. 10; Matches 15; Conservative 5; Mismatches 16; Indels 0; Gaps 0;  
 Db 146 PPPALPAPPPVPASTPARTLAKTPTPSAPAVKSA 181  
  
**RESULT 13**  
 C75286 hypothetical protein - Deinococcus radiodurans (strain R1)  
 C;Species: Deinococcus radiodurans  
 C;Accession: C75286  
 C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 R;White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
 S.; Smith, H.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
 Science 286, 1571-1577, 1999  
 A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
 A;Reference number: A75250; MUBD:20036896; PMID:10567266  
 A;Accession: C75286  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-559 <WHI>  
 A;Cross-references: UNIPROT:Q9R94; GB:AE002065; GB:AE000513; NID:96460149; PIDN:AAF1189  
 A;Experimental source: strain R1  
 C;Genetics:  
 A;Gene: DR2348  
 A;Map position: 1  
 C;Superfamily: Deinococcus radiodurans hypothetical protein DR2348  
 Query Match 24.5%; Score 70.5; DB 2; Length 559;  
 Best Local Similarity 35.7%; Pred. No. 23; Matches 20; Conservative 4; Mismatches 15; Indels 17; Gaps 2;  
 Db 1 PRASALPAPPTGSAIPDPQTASAIPD-----PRAS--ALPAALAV 39  
 258 PATSGGAPASPDTTIPDPATATDGGTSGAGDLTPPGVTEQMPPAATEPAPAPA 313  
  
**RESULT 14**  
 Q8BE3 BHLF1 protein - human herpesvirus 4 (strain B95-8)  
 C;Species: human herpesvirus 4, Epstein-Barr virus  
 C;Date: 25-Feb-1985 #sequence\_revision 25-Feb-1985 #text\_change 09-Jul-2004  
 C;Accession: A03742  
 R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.  
 Mol. Biol. Med. 1, 2145, 1983

A;Title: Sequence analysis of the 17/166 bp EcoRI fragment C of B95-8 Epstein-Barr virus.  
 A;Accession: A03424  
 A;Residues: 1-660 <BAN>  
 A;Cross-references: UNIPROT:P03181  
 R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; He  
 Nature 310, 207-211, 1984  
 A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.  
 A;Reference number: A03794; MUID:8420767; PMID:6087149  
 A;Contents: annotation; protein coding region  
 A;Comment: The sequence contains four perfect repeats (residues 149-273, 274-398, 399-52:  
 C;Superfamily: human herpesvirus 4 BHlf1 protein  
  
 Query Match 24.5%; Score 70.5; DB 1; Length 660;  
 Best Local Similarity 41.0%; Pred. No. 27;  
 Matches 16; Conservative 4; Mismatches 14; Indels 5; Gaps 1;  
 Qy 1 PRASALPAPPTGALPD-----POTASALPDPPAASALP 34  
 Db 192 PGTPAPGPGGAAVPSCATPHPERGSGPADPPAARLP 230  
  
 RESULT 15  
 T14150 vesicle associated protein 1 - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
 C;Accession: T14150  
 R;Shugrue, C.A.; Peters, H.; Matovcik, L.M.; Kolen, E.R.; Czernik, A.J.; Hubbard, A.; Gor  
 submitted to the EMBL Data Library, November 1997  
 A;Reference number: Z17887  
 A;Accession: T14150  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: mRNA  
 A;Residues: 1-1249 <SHU>  
 A;Cross-references: UNIPROT:Q9ZQ1; EMBL:AF034582; NID:94104320; PID:94104321; PNID:AAD01  
 A;Experimental source: liver  
 A;Genetics:  
 A;Gene: VAP1  
  
 Query Match 24.1%; Score 69.5; DB 2; Length 1249;  
 Best Local Similarity 37.3%; Pred. No. 61; Gaps 2;  
 Matches 19; Conservative 37.3%; Pred. No. 61; Gaps 2;  
 Mismatches 4; Indels 15; Gaps 2;  
 Qy 1 PRASALPAPPT-----GSAALPDOTASALP-----DPPAASALPAA 36  
 Db 965 PTSSSAPLPPPPSSGGASFOHGGPGAPPSSAYALPPGTGTGTPRASELPAS 1015  
  
 Search completed: March 7, 2005, 07:21:01  
 Job time : 6.8765 secs